

SEQUENCE LISTING

<110> Ruey S. Liou

<120> ANTI-IGE GENE THERAPY

<130> 99-5

<150> 60/100,639

<151> 1998-09-16

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21

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<213> primer

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ctgagctcac ggtcaccag

19

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<211> 21

<212> DNA

<213> primer

<400> 3

tccgacatcc tgctgaccca g

21

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<211> 19

<212> DNA

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<400> 4

gtttgatctc caccttggt

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<213> primer

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gatctgacat cctgctgacc cagag

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ggggs ggggs ggggs

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gctgatctcg cccacccact cc

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cccgagatct cgagtcattt gatctccacc

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ggagatctcc acagtccttg aacacac

27

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29

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cggaattcga gcggatgctg caccaactgt atcgatct

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tgagctcacg gtcaccaggg t

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<400> 22
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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agc gtg aag gtg agc tgc aag gcc agc ggc tac acc ttc agc atg tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Met Tyr
20 25 30

tgg ctg gag tgg gtg agg cag gcc ccc ggc cac ggc ctg gag tgg gtg 144
Trp Leu Glu Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Val
35 40 45

ggc gag atc agc ccc ggc acc ttc acc acc aac tac aac gag aag ttc 192
Gly Glu Ile Ser Pro Gly Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

aag gcc agg gcc acc ttc acc gcc gac acc agc acc aac acc gcc tac 240
Lys Ala Arg Ala Thr Phe Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

atg gag ctg agc agc ctg agg agc gag gac acc gcc gtg tac tac tgc 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcc agg ttc agc cac ttc agc ggc agc aac tac gac tac ttc gac tac 336
Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

tgg ggc cag ggc acc ctg gtg acc gtg agc tca 369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

<210> 23
 <211> 122
 <212> PRT
 <213> human/murine

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Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
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Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Met	Tyr	
			20					25					30			
Trp	Leu	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	His	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Gly	Glu	Ile	Ser	Pro	Gly	Thr	Phe	Thr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	
	50					55				60						
Lys	Ala	Arg	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Thr	Asn	Thr	Ala	Tyr	
65					70				75						80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
Ala	Arg	Phe	Ser	His	Phe	Ser	Gly	Ser	Asn	Tyr	Asp	Tyr	Phe	Asp	Tyr	
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Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser							
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 <212> DNA
 <213> human/murine

<220>

<221> CDS

<222> (1)...(321)

<400> 24

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Asp	Ile	Leu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5				10						15		
gag	agg	gcc	acc	ctg	agc	tgc	agg	gcc	agc	cag	agc	atc	ggc	acc	aac	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	
			20					25					30			
atc	cac	tgg	tac	cag	cag	aag	ccc	ggc	cag	gcc	ccc	agg	ctg	ctg	atc	144
Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	
		35					40					45				
aag	tac	gcc	agc	gag	agc	atc	agc	ggc	atc	ccc	agc	agg	ttc	agc	ggc	192
Lys	Tyr	Ala	Ser	Glu	Ser	Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						
agc	ggc	agc	ggc	acc	gac	ttc	acc	ctg	acc	atc	agc	agg	ctg	gag	ccc	240
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	
65					70					75					80	
gag	gac	ttc	gcc	atg	tac	tac	tgc	cag	cag	agc	gac	agc	tgg	ccc	acc	288
Glu	Asp	Phe	Ala	Met	Tyr	Tyr	Cys	Gln	Gln	Ser	Asp	Ser	Trp	Pro	Thr	
				85						90				95		

atg gag ctg agc agc ctg agg agc gag gac acc gcc gtg tac tac tgc	288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcc agg ttc agc cac ttc agc ggc agc aac tac gac tac ttc gac tac	336
Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr	
100 105 110	
tgg ggc cag ggc acc ctg gtg acc gtg agc tca ggt ggc ggt ggc tcg	384
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser	
115 120 125	
ggc ggt ggt ggc tgc ggt ggc ggc gga tct gac atc ctg ctg acc cag	432
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Leu Leu Thr Gln	
130 135 140	
agc ccc ggc acc ctg agc ctg agc ccc ggc gag agg gcc acc ctg agc	480
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser	
145 150 155 160	
tgc agg gcc agc cag agc atc ggc acc aac atc cac tgg tac cag cag	528
Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln	
165 170 175	
aag ccc ggc cag gcc ccc agg ctg ctg atc aag tac gcc agc gag agc	576
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser	
180 185 190	
atc agc ggc atc ccc agc agg ttc agc ggc agc ggc agc ggc acc gac	624
Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
195 200 205	
ttc acc ctg acc atc agc agg ctg gag ccc gag gac ttc gcc atg tac	672
Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Met Tyr	
210 215 220	
tac tgc cag cag agc gac agc tgg ccc acc acc ttc ggc cag ggc acc	720
Tyr Cys Gln Gln Ser Asp Ser Trp Pro Thr Thr Phe Gly Gln Gly Thr	
225 230 235 240	
aag gtg gag atc aaa	735
Lys Val Glu Ile Lys	
245	

<210> 27

<211> 245

<212> PRT

<213> human/murine

<400> 27

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Met Tyr	
20 25 30	
Trp Leu Glu Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Val	
35 40 45	

[illegible]